SEQUENCE LISTING

<110> Walke, D. Wade
Hu, Yi
Nepomnichy, Boris
Turner, C. Alexander Jr
Zambrowicz, Brian

<120> Novel Human Kinases and Polynucleotides Encoding the Same

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<150> US 60/183,582
<151> 2000-02-18

<150> US 60/184,014
<151> 2000-02-22

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<212> PRT
<213> homo sapiens

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Gly Phe Ile Ala Lys Arg Ile Glu Lys Phe Leu Ser Pro Gln Leu Ile
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Ala Glu Glu Phe Cys Leu Lys Thr Phe Ser Lys Phe Gly Ser Gln Pro
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Ile Pro Ala Lys Arg Pro Ala Ser Gly Gln Asn Ser Ile Ser Val Met
                85                  90                  95
Pro Ala Gln Lys Ile Thr Lys Pro Ala Ala Lys Tyr Gly Ile Pro Leu
            100                 105                 110
Ala Tyr Lys Lys Tyr Gly Asp Lys Lys Leu His Glu Lys Lys Pro Leu
        115                 120                 125
Gln Lys His Lys Gln Ala His Gln Thr Pro Glu Lys Arg Val Asn Thr
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Gly Glu Glu Arg Arg Lys Ile Ser Glu Glu Ala Ala Arg Lys Arg Arg
145                 150                 155                 160
Leu Glu Phe Ile Glu Lys Glu Lys Lys Gln Lys Asp Gln Ile Ile Ser
                165                 170                 175
Leu Met Lys Ala Glu Gln Met Lys Arg Gln Glu Lys Glu Arg Leu Glu
            180                 185                 190
Arg Ile Asn Arg Ala Arg Glu Gln Gly Trp Arg Asn Val Leu Ser Ala
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Gly Gly Ser Gly Glu Val Lys Ala Pro Phe Leu Gly Ser Gly Gly Thr
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Ile Ala Pro Ser Ser Phe Ser Ser Arg Gly Gln Tyr Glu His Tyr His
225                 230                 235                 240
Ala Ile Phe Asp Gln Met Gln Gln Gln Arg Ala Glu Asp Asn Glu Ala
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Lys Trp Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys
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Gly Gln Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln
        275                 280                 285
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Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu Arg Gln Gln Ile
            340                 345                 350
Lys Ala Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn His Ser Glu Gly
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Gln Glu Gly Ser Glu Glu Ala Asp Met Arg Arg Lys Lys Ile Glu Ser
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Glu His Leu Val Ala Lys Gly Val Lys Ser Ser Asp Val Ser Pro Pro
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Leu Gly Gln His Glu Thr Gly Gly Ser Pro Ser Lys Gln Gln Met Arg
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Leu Lys Ala Gln Glu Asp Glu Lys Gly Met Gln Asn Leu Ser Asp Thr
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Phe Glu Ile Asn Val His Glu Asp Ala Lys Glu His Glu Lys Glu Lys
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Ser Val Ser Ser Asp Arg Lys Lys Trp Glu Ala Gly Gly Gln Leu Val
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Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn Gly Ser Pro
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Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly Thr Asn Lys
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Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile Ser Glu Glu
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Lys Glu Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile Thr Ile Gln Glu
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Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp Gln Leu Ser
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Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln His Ser Lys Cys
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Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His Lys Val Val
        755                 760                 765
His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln Ser Val Gln Cys
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Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser His Leu Pro Pro
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Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr Val Gly Asp
        835                 840                 845
Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp Glu Asn Ile
    850                 855                 860
Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu Glu Thr Asp
865                 870                 875                 880
Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu Leu Arg Glu
                885                 890                 895
Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Glu Ser Val Leu Lys Asn
            900                 905                 910
Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala Asp Glu Asp
        915                 920                 925
Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp His Ser Asp
    930                 935                 940
Asn Ser Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys Asp Ser Val Phe
945                 950                 955                 960
Asn His Leu Glu Glu Leu Arg Leu His Leu Glu Gln Glu Met Gly Phe
                965                 970                 975
Glu Lys Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala Ile His Glu Asp
            980                 985                 990
Glu Asp Glu Asn Ile Glu Ile Cys Ser Lys Ile Val Gln Asn Ile Leu
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<212> PRT
<213> homo sapiens

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Arg Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val
    50                  55                  60
Gln Tyr Arg Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met
65                  70                  75                  80
Asp Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys
                85                  90                  95
Gly Val Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile
            100                 105                 110
Cys Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp
        115                 120                 125
Ile Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu
    130                 135                 140
Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala
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Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu
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        195                 200                 205
Lys Asn Leu Val Leu Lys Ile Ile Ser Gly Ser Phe Pro Pro Val Ser
    210                 215                 220
Leu His Tyr Ser Tyr Asp Leu Arg Ser Leu Val Ser Gln Leu Phe Lys
225                 230                 235                 240
Arg Asn Pro Arg Asp Arg Pro Ser Val Asn Ser Ile Leu Glu Lys Gly
                245                 250                 255
Phe Ile Ala Lys Arg Ile Glu Lys Phe Leu Ser Pro Gln Leu Ile Ala
            260                 265                 270
Glu Glu Phe Cys Leu Lys Thr Phe Ser Lys Phe Gly Ser Gln Pro Ile
        275                 280                 285
Pro Ala Lys Arg Pro Ala Ser Gly Gln Asn Ser Ile Ser Val Met Pro
    290                 295                 300
Ala Gln Lys Ile Thr Lys Pro Ala Ala Lys Tyr Gly Ile Pro Leu Ala
305                 310                 315                 320
Tyr Lys Lys Tyr Gly Asp Lys Lys Leu His Glu Lys Lys Pro Leu Gln
                325                 330                 335
Lys His Lys Gln Ala His Gln Thr Pro Glu Lys Arg Val Asn Thr Gly
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Glu Glu Arg Arg Lys Ile Ser Glu Glu Ala Ala Arg Lys Arg Arg Leu
        355                 360                 365
Glu Phe Ile Glu Lys Glu Lys Lys Gln Lys Asp Gln Ile Ile Ser Leu
    370                 375                 380
Met Lys Ala Glu Gln Met Lys Arg Gln Glu Lys Glu Arg Leu Glu Arg
385                 390                 395                 400
Ile Asn Arg Ala Arg Glu Gln Gly Trp Arg Asn Val Leu Ser Ala Gly
                405                 410                 415
Gly Ser Gly Glu Val Lys Ala Pro Phe Leu Gly Ser Gly Gly Thr Ile
            420                 425                 430
Ala Pro Ser Ser Phe Ser Ser Arg Gly Gln Tyr Glu His Tyr His Ala
        435                 440                 445
Ile Phe Asp Gln Met Gln Gln Gln Arg Ala Glu Asp Asn Glu Ala Lys
    450                 455                 460
Trp Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys Gly
465                 470                 475                 480
Gln Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln Arg
                485                 490                 495
Lys Arg Glu Ala Met Gln Asn Lys Ala Arg Ala Glu Gly His Met Val
            500                 505                 510
Tyr Leu Ala Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu Arg
        515                 520                 525
Gln Gln Ile Lys Ala Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn His
    530                 535                 540
Ser Glu Gly Gln Glu Gly Ser Glu Glu Ala Asp Met Arg Arg Lys Lys
545                 550                 555                 560
Ile Glu Ser Leu Lys Ala His Ala Asn Ala Arg Ala Ala Val Leu Lys
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Glu Gln Leu Glu Arg Lys Arg Lys Glu Ala Tyr Glu Arg Glu Lys Lys
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Val Trp Glu Glu His Leu Val Ala Lys Gly Val Lys Ser Ser Asp Val
        595                 600                 605
Ser Pro Pro Leu Gly Gln His Glu Thr Gly Gly Ser Pro Ser Lys Gln
    610                 615                 620
Gln Met Arg Ser Val Ile Ser Val Thr Ser Ala Leu Lys Glu Val Gly
625                 630                 635                 640
Val Asp Ser Ser Leu Thr Asp Thr Arg Glu Thr Ser Glu Glu Met Gln
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Lys Thr Asn Asn Ala Ile Ser Ser Lys Arg Glu Ile Leu Arg Arg Leu
            660                 665                 670
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Ser Asp Thr Phe Glu Ile Asn Val His Glu Asp Ala Lys Glu His Glu
690 695 700
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705 710 715 720
Gln Leu Val Ile Pro Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe Ser
725 730 735
Thr Thr Glu Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn
740 745 750
Gly Ser Pro Arg Arg Ala Trp Gly Lys Ser Pro Thr Asp Ser Val Leu
755 760 765
Lys Ile Leu Gly Glu Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu Glu
770 775 780
Asn Thr Thr Ile Arg Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr Lys
785 790 795 800
Pro Leu Ile Thr Gly Glu Lys Lys Val Gln Cys Ile Ser His Glu Ile
805 810 815
Asn Pro Ser Ala Ile Val Asp Ser Pro Val Glu Thr Lys Ser Pro Glu
820 825 830
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Glu Glu Pro Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly
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Thr Asn Lys Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile
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885 890 895
Ile Gln Glu Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp
900 905 910
Gln Leu Ser Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln His
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Ser Lys Cys Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His
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Lys Val Val His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln Ser
945 950 955 960
Val Gln Cys Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser His
965 970 975
Leu Pro Pro Lys Asn Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu Ser
980 985 990
Thr Gly Leu Phe Asp Ala Asn Asn Pro Lys Met Leu Arg Thr Cys Ser
995 1000 1005
Leu Pro Asp Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr
1010 1015 1020
Val Gly Asp Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp
1025 1030 1035 1040
Glu Asn Ile Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu
1045 1050 1055
Glu Thr Asp Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu
1060 1065 1070
Leu Arg Glu Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Glu Ser Val
1075 1080 1085
Leu Lys Asn Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala
1090 1095 1100
Asp Glu Asp Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp
1105 1110 1115 1120
His Ser Asp Asn Ser Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys Asp
1125 1130 1135
Ser Val Phe Asn His Leu Glu Glu Leu Arg Leu His Leu Glu Gln Glu
1140 1145 1150
Met Gly Phe Glu Lys Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala Ile
1155 1160 1165
His Glu Asp Glu Asp Glu Asn Ile Glu Ile Cys Ser Lys Ile Val Gln

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    1170                1175                1180
Asn Ile Leu Gly Asn Glu His Gln His Leu Tyr Ala Lys Ile Leu His
1185                1190                1195                1200
Leu Val Met Ala Asp Gly Ala Tyr Gln Glu Asp Asn Asp Glu
                1205                1210
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<210> 5
<211> 3024
<212> DNA
<213> homo sapiens

<400> 5

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tcctatgatc tccgcagttt ggtgtctcag ttatttaaaa gaaatcctag ggatagacca     120
tcagtcaact ccatattgga gaaaggtttt atagccaaac gcattgaaaa gtttctctct     180
cctcagctta ttgcagaaga attttgtcta aaaacatttt cgaagtttgg atcacagcct     240
ataccagcta aaagaccagc ttcaggacaa aactcgattt ctgttatgcc tgctcagaaa     300
attacaaagc ctgccgctaa atatggaata cctttagcat ataagaaata tggagataaa     360
aaattacacg aaaagaaacc actgcaaaaa cataaacagg cccatcaaac tccagagaag     420
agagtgaata ctggagaaga aaggaggaaa atatctgagg aagcagcaag aaagagaagg     480
ctggaattta ttgaaaaaga aaagaaacaa aaggatcaga ttattagttt aatgaaggct     540
gaacaaatga aaaggcaaga aaaggaaagg ttggaaagaa taaatagggc cagggaacaa     600
ggatggagaa atgtgctaag tgctggtgga agtggtgaag taaaggctcc ttttctgggc     660
agtggaggga ctatagctcc atcatctttt tcttctcgag gacagtatga acattaccat     720
gccatttttg accaaatgca gcaacaaaga gcagaagata atgaagctaa atggaaaaga     780
gaaatatatg gtcgaggtct tccagaaagg caaaaagggc agctagctgt agaaagagct     840
aaacaagtag aagagttcct gcagcgaaaa cgggaagcta tgcagaataa agctcgagcc     900
gaaggacata tggtttatct ggcaagactg aggcaaataa gactacagaa tttcaatgag     960
cgccaacaga ttaaagccaa acttcgtggt gaaaagaaag aagctaatca ttctgaagga    1020
caagaaggaa gtgaagaggc tgacatgagg cgcaaaaaaa tcgaatcact gaaggcccat    1080
gcaaatgcac gtgctgctgt actaaaagaa caactagaac gaaagagaaa ggaggcttat    1140
gagagagaaa aaaaagtgtg ggaagagcat ttggtggcta aaggagttaa gagttctgat    1200
gtttctccac ctttgggaca gcatgaaaca ggtggctctc catcaaagca acagatgaga    1260
tctgttattt ctgtaacttc agctttgaaa gaagttggcg tggacagtag tttaactgat    1320
acccgggaaa cttcagaaga gatgcaaaag accaacaatg ctatttcaag taagcgagaa    1380
atacttcgca gattaaatga aaatcttaaa gctcaagaag atgaaaaagg aatgcagaat    1440
ctctctgata cttttgagat aaatgttcat gaagatgcca aagagcatga aaaagaaaaa    1500
tcagtttcat ctgatcgcaa gaagtgggag gcaggaggtc aacttgtgat tcctctggat    1560
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ctaaagatac ttggagaagc tgaactacaa cttcagacag aactattaga aaatacaact    1740
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acaaaaagtc ccgagttcag tgaggcatct ccacagatgt cattgaaact ggaaggaaat    1920
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gatgagagct tgccatgcac tattactgat gtgtggatta gtgaggaaaa agaaacaaag    2040
gaaactcagt cggcagatag gatcaccatt caggaaaatg aagtttctga agatggagtc    2100
tcgagtactg tggaccaact tagtgacatt catatagagc ctggaaccaa tgattctcag    2160
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tcacttccag atctctcaaa gctgttcaga acccttatgg atgttcccac cgtaggagat    2460
gttcgtcaag acaatcttga aatagatgaa attaaagatg aaaacattaa agaaggacct    2520
tctgattctg aagacattgt gtttgaagaa actgacacag atttacaaga gctgcaggcc    2580
tcgatggaac agttacttag ggaacaacct ggtgaagaat acagtgaaga agaagagtca    2640
gtcttgaaga acagtgatgt ggagccaact gcaaatggga cagatgtggc agatgaagat    2700
gacaatccca gtagtgaaag tgccctgaac gaagaatggc actcagataa cagtgatggt    2760
gaaattgcta gtgaatgtga atgcgatagt gtctttaacc atttagagga actgagactt    2820
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attcatgaag atgaagatga aaatattgaa atttgttcaa aaatagttca aaatattttg    2940
ggaaatgaac atcagcatct ttatgccaag attcttcatt tagtcatggc agatggagcc    3000
taccaagaag ataatgatga ataa                                            3024
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<210> 6
<211> 1007
<212> PRT
<213> homo sapiens

<400> 6
Met Lys Asn Leu Val Leu Lys Ile Ile Ser Gly Ser Phe Pro Pro Val
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Ser Leu His Tyr Ser Tyr Asp Leu Arg Ser Leu Val Ser Gln Leu Phe
            20   25   30
Lys Arg Asn Pro Arg Asp Arg Pro Ser Val Asn Ser Ile Leu Glu Lys
        35   40   45
Gly Phe Ile Ala Lys Arg Ile Glu Lys Phe Leu Ser Pro Gln Leu Ile
    50   55   60
Ala Glu Glu Phe Cys Leu Lys Thr Phe Ser Lys Phe Gly Ser Gln Pro
65   70   75   80
Ile Pro Ala Lys Arg Pro Ala Ser Gly Gln Asn Ser Ile Ser Val Met
                85   90   95
Pro Ala Gln Lys Ile Thr Lys Pro Ala Ala Lys Tyr Gly Ile Pro Leu
            100   105   110
Ala Tyr Lys Lys Tyr Gly Asp Lys Lys Leu His Glu Lys Lys Pro Leu
        115   120   125
Gln Lys His Lys Gln Ala His Gln Thr Pro Glu Lys Arg Val Asn Thr
    130   135   140
Gly Glu Glu Arg Arg Lys Ile Ser Glu Glu Ala Ala Arg Lys Arg Arg
145   150   155   160
Leu Glu Phe Ile Glu Lys Glu Lys Lys Gln Lys Asp Gln Ile Ile Ser
                165   170   175
Leu Met Lys Ala Glu Gln Met Lys Arg Gln Glu Lys Glu Arg Leu Glu
            180   185   190
Arg Ile Asn Arg Ala Arg Glu Gln Gly Trp Arg Asn Val Leu Ser Ala
        195   200   205
Gly Gly Ser Gly Glu Val Lys Ala Pro Phe Leu Gly Ser Gly Gly Thr
    210   215   220
Ile Ala Pro Ser Ser Phe Ser Ser Arg Gly Gln Tyr Glu His Tyr His
225   230   235   240
Ala Ile Phe Asp Gln Met Gln Gln Gln Arg Ala Glu Asp Asn Glu Ala
                245   250   255
Lys Trp Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys
            260   265   270
Gly Gln Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln
        275   280   285
Arg Lys Arg Glu Ala Met Gln Asn Lys Ala Arg Ala Glu Gly His Met
    290   295   300
Val Tyr Leu Ala Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu
305   310   315   320
Arg Gln Gln Ile Lys Ala Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn
                325   330   335
His Ser Glu Gly Gln Glu Gly Ser Glu Glu Ala Asp Met Arg Arg Lys
            340   345   350
Lys Ile Glu Ser Leu Lys Ala His Ala Asn Ala Arg Ala Ala Val Leu
        355   360   365
Lys Glu Gln Leu Glu Arg Lys Arg Lys Glu Ala Tyr Glu Arg Glu Lys
    370   375   380
Lys Val Trp Glu Glu His Leu Val Ala Lys Gly Val Lys Ser Ser Asp
385   390   395   400
Val Ser Pro Pro Leu Gly Gln His Glu Thr Gly Gly Ser Pro Ser Lys
                405   410   415
Gln Gln Met Arg Ser Val Ile Ser Val Thr Ser Ala Leu Lys Glu Val
            420   425   430
Gly Val Asp Ser Ser Leu Thr Asp Thr Arg Glu Thr Ser Glu Glu Met
        435   440   445
Gln Lys Thr Asn Asn Ala Ile Ser Ser Lys Arg Glu Ile Leu Arg Arg

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    450                 455                 460
Leu Asn Glu Asn Leu Lys Ala Gln Glu Asp Glu Lys Gly Met Gln Asn
465                 470                 475                 480
Leu Ser Asp Thr Phe Glu Ile Asn Val His Glu Asp Ala Lys Glu His
                485                 490                 495
Glu Lys Glu Lys Ser Val Ser Ser Asp Arg Lys Lys Trp Glu Ala Gly
            500                 505                 510
Gly Gln Leu Val Ile Pro Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe
        515                 520                 525
Ser Thr Thr Glu Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro
    530                 535                 540
Asn Gly Ser Pro Arg Arg Ala Trp Gly Lys Ser Pro Thr Asp Ser Val
545                 550                 555                 560
Leu Lys Ile Leu Gly Glu Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu
                565                 570                 575
Glu Asn Thr Thr Ile Arg Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr
            580                 585                 590
Lys Pro Leu Ile Thr Gly Glu Lys Lys Val Gln Cys Ile Ser His Glu
        595                 600                 605
Ile Asn Pro Ser Ala Ile Val Asp Ser Pro Val Glu Thr Lys Ser Pro
    610                 615                 620
Glu Phe Ser Glu Ala Ser Pro Gln Met Ser Leu Lys Leu Glu Gly Asn
625                 630                 635                 640
Leu Glu Glu Pro Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser
                645                 650                 655
Gly Thr Asn Lys Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp
            660                 665                 670
Ile Ser Glu Glu Lys Glu Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile
        675                 680                 685
Thr Ile Gln Glu Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val
    690                 695                 700
Asp Gln Leu Ser Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln
705                 710                 715                 720
His Ser Lys Cys Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe
                725                 730                 735
His Lys Val Val His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln
            740                 745                 750
Ser Val Gln Cys Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser
        755                 760                 765
His Leu Pro Pro Lys Asn Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu
    770                 775                 780
Ser Thr Gly Leu Phe Asp Ala Asn Asn Pro Lys Met Leu Arg Thr Cys
785                 790                 795                 800
Ser Leu Pro Asp Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro
                805                 810                 815
Thr Val Gly Asp Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys
            820                 825                 830
Asp Glu Asn Ile Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe
        835                 840                 845
Glu Glu Thr Asp Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln
    850                 855                 860
Leu Leu Arg Glu Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Glu Ser
865                 870                 875                 880
Val Leu Lys Asn Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val
                885                 890                 895
Ala Asp Glu Asp Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu
            900                 905                 910
Trp His Ser Asp Asn Ser Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys
        915                 920                 925
Asp Ser Val Phe Asn His Leu Glu Glu Leu Arg Leu His Leu Glu Gln
    930                 935                 940
Glu Met Gly Phe Glu Lys Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala
945                 950                 955                 960
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Ile His Glu Asp Glu Asp Glu Asn Ile Glu Ile Cys Ser Lys Ile Val
                965                 970                 975
Gln Asn Ile Leu Gly Asn Glu His Gln His Leu Tyr Ala Lys Ile Leu
            980                 985                 990
His Leu Val Met Ala Asp Gly Ala Tyr Gln Glu Asp Asn Asp Glu
        995                 1000                1005
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<210> 7
<211> 891
<212> DNA
<213> homo sapiens

<400> 7

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atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat     180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc     240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca     300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac     360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc     420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg     480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat     540
gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa     600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc     660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat     720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat     780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat     840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggtg a               891
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<210> 8
<211> 296
<212> PRT
<213> homo sapiens

<400> 8

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Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
 1               5                  10                  15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
            20                  25                  30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
        35                  40                  45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
    50                  55                  60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65                  70                  75                  80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
                85                  90                  95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
            100                 105                 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
        115                 120                 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
    130                 135                 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145                 150                 155                 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
                165                 170                 175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
            180                 185                 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
        195                 200                 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
```

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    210                 215                 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225                 230                 235                 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
                245                 250                 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
            260                 265                 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
        275                 280                 285
Pro Ser Lys His Phe Gln Glu Arg
    290                 295
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<210> 9
<211> 219
<212> DNA
<213> homo sapiens

<400> 9
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aaggcaattc catgtaagga agctgggctt tctttcaaaa agggagatat tcttcagatt 120
atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg 180
gcaggcttga tcccctcaaa gcatttccag gaaaggtga 219

<210> 10
<211> 72
<212> PRT
<213> homo sapiens

<400> 10
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Met Lys Leu Phe Phe Gln Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
 1               5                  10                  15
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
            20                  25                  30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35                  40                  45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50                  55                  60
Pro Ser Lys His Phe Gln Glu Arg
65                  70
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<210> 11
<211> 957
<212> DNA
<213> homo sapiens

<400> 11
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atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540
gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa 600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc 660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat 720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat 780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat 840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900
agacgaccag aaatattggt tcagcccctg aaagtttcca acaggaaatc atcctaa 957

<210> 12
<211> 318
<212> PRT
<213> homo sapiens

<400> 12
Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
 1   5   10   15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
            20   25   30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
        35   40   45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
    50   55   60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65   70   75   80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
                85   90   95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
            100   105   110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
        115   120   125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
    130   135   140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145   150   155   160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
                165   170   175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
            180   185   190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
        195   200   205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
    210   215   220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225   230   235   240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
                245   250   255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
            260   265   270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
        275   280   285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
    290   295   300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser
305   310   315

<210> 13
<211> 285
<212> DNA
<213> homo sapiens

<400> 13
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atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg 180
gcaggcttga tccccctcaaa gcatttccag gaaaggagat tggctttgag acgaccagaa 240
atattggttc agcccctgaa agtttccaac aggaaatcat cctaa 285

<210> 14
<211> 94
<212> PRT
<213> homo sapiens

<400> 14
Met Lys Leu Phe Phe Gln Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
 1   5   10   15
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
            20   25   30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35   40   45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50   55   60
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
65   70   75   80
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser
                85   90

<210> 15
<211> 327
<212> DNA
<213> homo sapiens

<400> 15
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cgaaagctgc tgatcagtga cacccagcac tatggcgtga cagtgcccca taccaccaga 120
gcaagaagaa gccaggagag tgatggtgtt gaatacattt tcatttccaa gcatttgttt 180
gagacagatg tacaaaataa caagtttatt gaatatggag aatataaaaa caactactac 240
ggcacaagta tagactcagt tcggtctgtc cttgctaaaa acaaagtttg tttgttggat 300
gttcagcctc atgtaagtaa acaatga   327

<210> 16
<211> 108
<212> PRT
<213> homo sapiens

<400> 16
Met Cys Cys Pro Lys Thr Ala Cys Arg Gly Pro Val Gly Val Gly Leu
 1   5   10   15
Asn Glu Leu Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly
            20   25   30
Val Thr Val Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp
        35   40   45
Gly Val Glu Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val
    50   55   60
Gln Asn Asn Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr
65   70   75   80
Gly Thr Ser Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val
                85   90   95
Cys Leu Leu Asp Val Gln Pro His Val Ser Lys Gln
            100   105

<210> 17
<211> 1128
<212> DNA
<213> homo sapiens

<400> 17
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ctgccagccc agctgcagcc acatgtggat agccaggaag acctgacctt cctctgggat 120
atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540

gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa 600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc 660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat 720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat 780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat 840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900
agacgaccag aaatattggt tcagcccctg aaagtttcca acaggaaatc atctggtttt 960
agaagaagtt ttcgtcttag tagaaaagat aagaaaacaa ataaatccat gtatgaatgc 1020
aagaagagtg atcagtacga cacagctgac gtacccacat acgaagaagt gacaccgtat 1080
cggcgacaaa ctaatgaaaa atacagactc gttgtcttgg ttgcttga 1128

<210> 18
<211> 375
<212> PRT
<213> homo sapiens

<400> 18
Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
1 5 10 15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
20 25 30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
35 40 45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
50 55 60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65 70 75 80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
85 90 95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
100 105 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
115 120 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
130 135 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145 150 155 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
165 170 175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
180 185 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
195 200 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
210 215 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225 230 235 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
245 250 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
260 265 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
275 280 285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
290 295 300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
305 310 315 320
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
325 330 335
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
340 345 350
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
355 360 365

Arg Leu Val Val Leu Val Ala
370 375

<210> 19
<211> 414
<212> DNA
<213> homo sapiens

<400> 19
atgtatgaat gcaagaagag tgatcagtac gacacagctg acgtacccac atacgaagaa 60
gtgacaccgt atcggcgaca aactaatgaa aaatacagac tcgttgtctt ggttggtccc 120
gtgggagtag ggctgaatga actgaaacga aagctgctga tcagtgacac ccagcactat 180
ggcgtgacag tgccccatac caccagagca agaagaagcc aggagagtga tggtgttgaa 240
tacattttca tttccaagca tttgtttgag acagatgtac aaaataacaa gtttattgaa 300
tatggagaat ataaaaacaa ctactacggc acaagtatag actcagttcg gtctgtcctt 360
gctaaaaaca aagtttgttt gttggatgtt cagcctcatg taagtaaaca atga 414

<210> 20
<211> 137
<212> PRT
<213> homo sapiens

<400> 20
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
1 5 10 15
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
20 25 30
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
35 40 45
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
50 55 60
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
65 70 75 80
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
85 90 95
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
100 105 110
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
115 120 125
Asp Val Gln Pro His Val Ser Lys Gln
130 135

<210> 21
<211> 1422
<212> DNA
<213> homo sapiens

<400> 21
atgccagctt tgtcaacggg atctgggagt gacactggtc tgtatgagct gttggctgct 60
ctgccagccc agctgcagcc acatgtggat agccaggaag acctgacctt cctctgggat 120
atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540
gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa 600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc 660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat 720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat 780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat 840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900

agacgaccag aaatattggt tcagcccctg aaagtttcca acaggaaatc atctggtttt 960
agaagaagtt ttcgtcttag tagaaaagat aagaaaacaa ataaatccat gtatgaatgc 1020
aagaagagtg atcagtacga cacagctgac gtacccacat acgaagaagt gacaccgtat 1080
cggcgacaaa ctaatgaaaa atacagactc gttgtcttgg ttggtcccgt gggagtaggg 1140
ctgaatgaac tgaaacgaaa gctgctgatc agtgacaccc agcactatgg cgtgacagtg 1200
ccccatacca ccagagcaag aagaagccag gagagtgatg gtgttgaata cattttcatt 1260
tccaagcatt tgtttgagac agatgtacaa aataacaagt ttattgaata tggagaatat 1320
aaaaacaact actacggcac aagtatagac tcagttcggt ctgtccttgc taaaaacaaa 1380
gtttgtttgt tggatgttca gcctcatgta agtaaacaat ga 1422

<210> 22
<211> 473
<212> PRT
<213> homo sapiens

<400> 22
Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
1 5 10 15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
20 25 30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
35 40 45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
50 55 60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65 70 75 80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
85 90 95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
100 105 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
115 120 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
130 135 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145 150 155 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
165 170 175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
180 185 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
195 200 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
210 215 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225 230 235 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
245 250 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
260 265 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
275 280 285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
290 295 300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
305 310 315 320
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
325 330 335
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
340 345 350
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
355 360 365
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu

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    370                 375                 380
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
385                 390                 395                 400
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
                405                 410                 415
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
            420                 425                 430
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
        435                 440                 445
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
    450                 455                 460
Asp Val Gln Pro His Val Ser Lys Gln
465                 470
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<210> 23
<211> 750
<212> DNA
<213> homo sapiens

<400> 23

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atgaaacttt tcttccagat gtttatcaaa gccctctttg actataatcc taatgaggat      60
aaggcaattc catgtaagga agctgggctt tctttcaaaa agggagatat tcttcagatt     120
atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg     180
gcaggcttga tcccctcaaa gcatttccag gaaaggagat tggctttgag acgaccagaa     240
atattggttc agcccctgaa agtttccaac aggaaatcat ctggttttag aagaagtttt     300
cgtcttagta gaaaagataa gaaaacaaat aaatccatgt atgaatgcaa gaagagtgat     360
cagtacgaca cagctgacgt acccacatac gaagaagtga caccgtatcg gcgacaaact     420
aatgaaaaat acagactcgt tgtcttggtt ggtcccgtgg gagtagggct gaatgaactg     480
aaacgaaagc tgctgatcag tgacacccag cactatggcg tgacagtgcc ccataccacc     540
agagcaagaa gaagccagga gagtgatggt gttgaataca ttttcatttc caagcatttg     600
tttgagacag atgtacaaaa taacaagttt attgaatatg gagaatataa aaacaactac     660
tacggcacaa gtatagactc agttcggtct gtccttgcta aaaacaaagt ttgtttgttg     720
gatgttcagc ctcatgtaag taaacaatga                                      750
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<210> 24
<211> 249
<212> PRT
<213> homo sapiens

<400> 24

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Met Lys Leu Phe Phe Gln Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
 1                5                  10                  15
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
            20                  25                  30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35                  40                  45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50                  55                  60
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
65                  70                  75                  80
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
                85                  90                  95
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
            100                 105                 110
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
        115                 120                 125
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
    130                 135                 140
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
145                 150                 155                 160
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
                165                 170                 175
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
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```
            180                 185                 190
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
        195                 200                 205
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
    210                 215                 220
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
225                 230                 235                 240
Asp Val Gln Pro His Val Ser Lys Gln
                245
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<210> 25
<211> 468
<212> DNA
<213> homo sapiens

<400> 25
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cgaaagctgc tgatcagtga cacccagcac tatggcgtga cagtgcccca taccaccaga 120
gcaagaagaa gccaggagag tgatggtgtt gaatacattt tcatttccaa gcatttgttt 180
gagacagatg tacaaaataa caagtttatt gaatatggag aatataaaaa caactactac 240
ggcacaagta tagactcagt tcggtctgtc cttgctaaaa acaaagtttg tttgttggat 300
gttcagcctc atacagtgaa gcatttaagg acactagaat ttaagcccta tgtgatattt 360
ataaagcctc catcaataga gcgtttgaga gaaacaagaa aaaatgcaaa gattatttca 420
agcagagatg accaaggtgc tgcaaaaccc ttcacacaag gagaatag 468

<210> 26
<211> 155
<212> PRT
<213> homo sapiens

<400> 26
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Met Cys Cys Pro Lys Thr Ala Cys Arg Gly Pro Val Gly Val Gly Leu
 1               5                  10                  15
Asn Glu Leu Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly
            20                  25                  30
Val Thr Val Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp
        35                  40                  45
Gly Val Glu Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val
    50                  55                  60
Gln Asn Asn Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr
65                  70                  75                  80
Gly Thr Ser Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val
                85                  90                  95
Cys Leu Leu Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu
            100                 105                 110
Glu Phe Lys Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg
        115                 120                 125
Leu Arg Glu Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp
    130                 135                 140
Gln Gly Ala Ala Lys Pro Phe Thr Gln Gly Glu
145                 150                 155
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<210> 27
<211> 555
<212> DNA
<213> homo sapiens

<400> 27
atgtatgaat gcaagaagag tgatcagtac gacacagctg acgtacccac atacgaagaa 60
gtgacaccgt atcggcgaca aactaatgaa aaatacagac tcgttgtctt ggttggtccc 120
gtgggagtag ggctgaatga actgaaaacga aagctgctga tcagtgacac ccagcactat 180
ggcgtgacag tgccccatac caccagagca agaagaagcc aggagagtga tggtgttgaa 240
tacattttca tttccaagca tttgtttgag acagatgtac aaaataacaa gtttattgaa 300

tatggagaat ataaaaacaa ctactacggc acaagtatag actcagttcg gtctgtcctt 360
gctaaaaaca aagtttgttt gttggatgtt cagcctcata cagtgaagca tttaaggaca 420
ctagaattta agccctatgt gatatttata aagcctccat caatagagcg tttgagagaa 480
acaagaaaaa atgcaaagat tatttcaagc agagatgacc aaggtgctgc aaaacccttc 540
acacaaggag aatag 555

<210> 28
<211> 184
<212> PRT
<213> homo sapiens

<400> 28
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
1 5 10 15
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
20 25 30
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
35 40 45
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
50 55 60
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
65 70 75 80
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
85 90 95
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
100 105 110
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
115 120 125
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
130 135 140
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
145 150 155 160
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
165 170 175
Ala Lys Pro Phe Thr Gln Gly Glu
180

<210> 29
<211> 1563
<212> DNA
<213> homo sapiens

<400> 29
atgccagctt tgtcaacggg atctgggagt gacactggtc tgtatgagct gttggctgct 60
ctgccagccc agctgcagcc acatgtggat agccaggaag acctgacctt cctctgggat 120
atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540
gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa 600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc 660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat 720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat 780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat 840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900
agacgaccag aaatattggt tcagcccctg aaagtttcca acaggaaatc atctggtttt 960
agaagaagtt ttcgtcttag tagaaaagat aagaaaacaa ataaatccat gtatgaatgc 1020
aagaagagtg atcagtacga cacagctgac gtacccacat acgaagaagt gacaccgtat 1080
cggcgacaaa ctaatgaaaa atacagactc gttgtcttgg ttggtcccgt gggagtaggg 1140
ctgaatgaac tgaaacgaaa gctgctgatc agtgacaccc agcactatgg cgtgacagtg 1200

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ccccatacca ccagagcaag aagaagccag gagagtgatg gtgttgaata cattttcatt    1260
tccaagcatt tgtttgagac agatgtacaa aataacaagt ttattgaata tggagaatat    1320
aaaaacaact actacggcac aagtatagac tcagttcggt ctgtccttgc taaaaacaaa    1380
gtttgtttgt tggatgttca gcctcataca gtgaagcatt taaggacact agaatttaag    1440
ccctatgtga tatttataaa gcctccatca atagagcgtt tgagagaaac aagaaaaaat    1500
gcaaagatta tttcaagcag agatgaccaa ggtgctgcaa aacccttcac acaaggagaa    1560
tag                                                                 1563
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<210> 30
<211> 520
<212> PRT
<213> homo sapiens

<400> 30

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Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
 1               5                  10                  15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
            20                  25                  30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
        35                  40                  45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
    50                  55                  60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65                  70                  75                  80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
                85                  90                  95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
            100                 105                 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
        115                 120                 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
    130                 135                 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145                 150                 155                 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
                165                 170                 175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
            180                 185                 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
        195                 200                 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
    210                 215                 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225                 230                 235                 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
                245                 250                 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
            260                 265                 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
        275                 280                 285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
    290                 295                 300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
305                 310                 315                 320
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
                325                 330                 335
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
            340                 345                 350
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
        355                 360                 365
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
    370                 375                 380
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
```

```
385                 390                 395                 400
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
                405                 410                 415
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
            420                 425                 430
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
        435                 440                 445
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
    450                 455                 460
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
465                 470                 475                 480
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
                485                 490                 495
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
            500                 505                 510
Ala Lys Pro Phe Thr Gln Gly Glu
        515                 520
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<210> 31
<211> 891
<212> DNA
<213> homo sapiens

<400> 31

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atgaaacttt tcttccagat gtttatcaaa gccctctttg actataatcc taatgaggat      60
aaggcaattc catgtaagga agctgggctt tctttcaaaa agggagatat tcttcagatt     120
atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg     180
gcaggcttga tcccctcaaa gcatttccag gaaaggagat tggctttgag acgaccagaa     240
atattggttc agcccctgaa agtttccaac aggaaatcat ctggttttag aagaagtttt     300
cgtcttagta gaaaagataa gaaaacaaat aaatccatgt atgaatgcaa gaagagtgat     360
cagtacgaca cagctgacgt acccacatac gaagaagtga caccgtatcg gcgacaaact     420
aatgaaaaat acagactcgt tgtcttggtt ggtcccgtgg gagtagggct gaatgaactg     480
aaacgaaagc tgctgatcag tgacacccag cactatggcg tgacagtgcc ccataccacc     540
agagcaagaa gaagccagga gagtgatggt gttgaataca ttttcatttc caagcatttg     600
tttgagacag atgtacaaaa taacaagttt attgaatatg gagaatataa aaacaactac     660
tacggcacaa gtatagactc agttcggtct gtccttgcta aaaacaaagt ttgtttgttg     720
gatgttcagc ctcatacagt gaagcattta aggacactag aatttaagcc ctatgtgata     780
tttataaagc ctccatcaat agagcgtttg agagaaacaa gaaaaaatgc aaagattatt     840
tcaagcagag atgaccaagg tgctgcaaaa cccttcacac aaggagaata g              891
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<210> 32
<211> 296
<212> PRT
<213> homo sapiens

<400> 32

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Met Lys Leu Phe Phe Gln Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
 1               5                  10                  15
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
            20                  25                  30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35                  40                  45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50                  55                  60
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
65                  70                  75                  80
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
                85                  90                  95
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
            100                 105                 110
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
        115                 120                 125
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
```

```
    130                 135                 140
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
145                 150                 155                 160
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
                165                 170                 175
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
            180                 185                 190
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
        195                 200                 205
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
    210                 215                 220
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
225                 230                 235                 240
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
                245                 250                 255
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
            260                 265                 270
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
        275                 280                 285
Ala Lys Pro Phe Thr Gln Gly Glu
    290                 295
```

<210> 33
<211> 585
<212> DNA
<213> homo sapiens

<400> 33
atgtgctgcc caaagactgc ttgcagaggt cccgtgggag tagggctgaa tgaactgaaa 60
cgaaagctgc tgatcagtga cacccagcac tatggcgtga cagtgcccca taccaccaga 120
gcaagaagaa gccaggagag tgatggtgtt gaatacattt tcatttccaa gcatttgttt 180
gagacagatg tacaaaataa caagtttatt gaatatggag aatataaaaa caactactac 240
ggcacaagta tagactcagt tcggtctgtc cttgctaaaa acaaagtttg tttgttggat 300
gttcagcctc atacagtgaa gcatttaagg acactagaat ttaagcccta tgtgatattt 360
ataaagcctc catcaataga gcgtttgaga gaaacaagaa aaaatgcaaa gattatttca 420
agcagagatg accaaggtgc tgcaaaaccc ttcacagaag aagattttca agaaatgatt 480
aaatctgcac agataatgga aagtcaatat ggtcatcttt ttgacaaaat tataataaat 540
gatgacctca ctgtggcatt caaaaaaaaa aaaaaaaaaa aaaaa 585

<210> 34
<211> 195
<212> PRT
<213> homo sapiens

<400> 34
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Met Cys Cys Pro Lys Thr Ala Cys Arg Gly Pro Val Gly Val Gly Leu
 1               5                  10                  15
Asn Glu Leu Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly
            20                  25                  30
Val Thr Val Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp
        35                  40                  45
Gly Val Glu Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val
    50                  55                  60
Gln Asn Asn Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr
65                  70                  75                  80
Gly Thr Ser Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val
                85                  90                  95
Cys Leu Leu Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu
            100                 105                 110
Glu Phe Lys Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg
        115                 120                 125
Leu Arg Glu Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp
    130                 135                 140
```

```
Gln Gly Ala Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile
145                 150                 155                 160
Lys Ser Ala Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys
                165                 170                 175
Ile Ile Ile Asn Asp Asp Leu Thr Val Ala Phe Lys Lys Lys Lys Lys
            180                 185                 190
Lys Lys Lys
        195
```

<210> 35
<211> 672
<212> DNA
<213> homo sapiens

<400> 35

```
atgtatgaat gcaagaagag tgatcagtac gacacagctg acgtacccac atacgaagaa      60
gtgacaccgt atcggcgaca aactaatgaa aaatacagac tcgttgtctt ggttggtccc     120
gtgggagtag ggctgaatga actgaaacga aagctgctga tcagtgacac ccagcactat     180
ggcgtgacag tgccccatac caccagagca agaagaagcc aggagagtga tggtgttgaa     240
tacattttca tttccaagca tttgtttgag acagatgtac aaaataacaa gtttattgaa     300
tatggagaat ataaaaacaa ctactacggc acaagtatag actcagttcg gtctgtcctt     360
gctaaaaaca aagtttgttt gttggatgtt cagcctcata cagtgaagca tttaaggaca     420
ctagaattta agccctatgt gatatttata aagcctccat caatagagcg tttgagagaa     480
acaagaaaaa atgcaaagat tatttcaagc agagatgacc aaggtgctgc aaaaccttc      540
acagaagaag attttcaaga aatgattaaa tctgcacaga taatggaaag tcaatatggt     600
catctttttg acaaaattat aataaatgat gacctcactg tggcattcaa aaaaaaaaaa     660
aaaaaaaaaa aa                                                         672
```

<210> 36
<211> 224
<212> PRT
<213> homo sapiens

<400> 36

```
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
 1               5                  10                  15
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
            20                  25                  30
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
        35                  40                  45
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
    50                  55                  60
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
65                  70                  75                  80
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
                85                  90                  95
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
            100                 105                 110
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
        115                 120                 125
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
    130                 135                 140
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
145                 150                 155                 160
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
                165                 170                 175
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
            180                 185                 190
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
        195                 200                 205
Asn Asp Asp Leu Thr Val Ala Phe Lys Lys Lys Lys Lys Lys Lys Lys
    210                 215                 220
```

<210> 37
<211> 1680
<212> DNA
<213> homo sapiens

<400> 37
atgccagctt tgtcaacggg atctgggagt gacactggtc tgtatgagct gttggctgct 60
ctgccagccc agctgcagcc acatgtggat agccaggaag acctgacctt cctctgggat 120
atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540
gttggtgatg aacttaggga agtcaacggg ataccagtgg aggataaaag gcctgaggaa 600
ataatacaga ttttggctca gtctcaggga gcaattacat ttaagattat acccggcagc 660
aaagaggaga caccatcaaa agaaggcaag atgtttatca aagccctctt tgactataat 720
cctaatgagg ataaggcaat tccatgtaag gaagctgggc tttctttcaa aaagggagat 780
attcttcaga ttatgagcca agatgatgca acttggtggc aagcgaaaca cgaagctgat 840
gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900
agacgaccag aaatattggt tcagcccctg aaagtttcca acaggaaatc atctggtttt 960
agaagaagtt ttcgtcttag tagaaaagat aagaaaacaa ataaatccat gtatgaatgc 1020
aagaagagtg atcagtacga cacagctgac gtacccacat acgaagaagt gacaccgtat 1080
cggcgacaaa ctaatgaaaa atacagactc gttgtcttgg ttggtcccgt gggagtaggg 1140
ctgaatgaac tgaaacgaaa gctgctgatc agtgacaccc agcactatgg cgtgacagtg 1200
ccccatacca ccagagcaag aagaagccag gagagtgatg gtgttgaata cattttcatt 1260
tccaagcatt tgtttgagac agatgtacaa aataacaagt ttattgaata tggagaatat 1320
aaaaacaact actacggcac aagtatagac tcagttcggt ctgtccttgc taaaaacaaa 1380
gtttgtttgt tggatgttca gcctcataca gtgaagcatt taaggacact agaatttaag 1440
ccctatgtga tatttataaa gcctccatca atagagcgtt tgagagaaac aagaaaaaat 1500
gcaaagatta tttcaagcag agatgaccaa ggtgctgcaa aacccttcac agaagaagat 1560
tttcaagaaa tgattaaatc tgcacagata atggaaagtc aatatggtca tctttttgac 1620
aaaattataa taaatgatga cctcactgtg gcattcaaaa aaaaaaaaaa aaaaaaaaaa 1680

<210> 38
<211> 560
<212> PRT
<213> homo sapiens

<400> 38
Met Pro Ala Leu Ser Thr Gly Ser Gly Ser Asp Thr Gly Leu Tyr Glu
1 5 10 15
Leu Leu Ala Ala Leu Pro Ala Gln Leu Gln Pro His Val Asp Ser Gln
20 25 30
Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
35 40 45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
50 55 60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65 70 75 80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
85 90 95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
100 105 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
115 120 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
130 135 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145 150 155 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
165 170 175

```
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
            180                 185                 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
        195                 200                 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
    210                 215                 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225                 230                 235                 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
                245                 250                 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
            260                 265                 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
        275                 280                 285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
    290                 295                 300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
305                 310                 315                 320
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
                325                 330                 335
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
            340                 345                 350
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
        355                 360                 365
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
    370                 375                 380
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
385                 390                 395                 400
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
                405                 410                 415
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
            420                 425                 430
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
        435                 440                 445
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
    450                 455                 460
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
465                 470                 475                 480
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
                485                 490                 495
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
            500                 505                 510
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
        515                 520                 525
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
    530                 535                 540
Asn Asp Asp Leu Thr Val Ala Phe Lys Lys Lys Lys Lys Lys Lys Lys
545                 550                 555                 560
```

<210> 39
<211> 1008
<212> DNA
<213> homo sapiens

<400> 39

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atgaaacttt tcttccagat gtttatcaaa gccctctttg actataatcc taatgaggat      60
aaggcaattc catgtaagga agctgggctt tctttcaaaa agggagatat tcttcagatt     120
atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg     180
gcaggcttga tcccctcaaa gcatttccag gaaaggagat tggctttgag acgaccagaa     240
atattggttc agcccctgaa agtttccaac aggaaatcat ctggttttag aagaagtttt     300
cgtcttagta gaaaagataa gaaaacaaat aaatccatgt atgaatgcaa gaagagtgat     360
cagtacgaca cagctgacgt acccacatac gaagaagtga caccgtatcg gcgacaaact     420
aatgaaaaat acagactcgt tgtcttggtt ggtcccgtgg gagtagggct gaatgaactg     480
```

```
aaacgaaagc tgctgatcag tgacacccag cactatggcg tgacagtgcc ccataccacc      540
agagcaagaa gaagccagga gagtgatggt gttgaataca ttttcatttc caagcatttg      600
tttgagacag atgtacaaaa taacaagttt attgaatatg gagaatataa aaacaactac      660
tacggcacaa gtatagactc agttcggtct gtccttgcta aaaacaaagt ttgtttgttg      720
gatgttcagc ctcatacagt gaagcattta aggacactag aatttaagcc ctatgtgata      780
tttataaagc ctccatcaat agagcgtttg agagaaacaa gaaaaaatgc aaagattatt      840
tcaagcagag atgaccaagg tgctgcaaaa cccttcacag aagaagattt tcaagaaatg      900
attaaatctg cacagataat ggaaagtcaa tatggtcatc tttttgacaa aattataata      960
aatgatgacc tcactgtggc attcaaaaaa aaaaaaaaaa aaaaaaaa                  1008
```

<210> 40
<211> 336
<212> PRT
<213> homo sapiens

<400> 40

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Met Lys Leu Phe Phe Gln Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
 1               5                  10                  15
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
            20                  25                  30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35                  40                  45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50                  55                  60
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
65                  70                  75                  80
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
                85                  90                  95
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
            100                 105                 110
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
        115                 120                 125
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
    130                 135                 140
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
145                 150                 155                 160
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
                165                 170                 175
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
            180                 185                 190
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
        195                 200                 205
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
    210                 215                 220
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
225                 230                 235                 240
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
                245                 250                 255
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
            260                 265                 270
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
        275                 280                 285
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
    290                 295                 300
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
305                 310                 315                 320
Asn Asp Asp Leu Thr Val Ala Phe Lys Lys Lys Lys Lys Lys Lys Lys
                325                 330                 335
```

<210> 41
<211> 636
<212> DNA
<213> homo sapiens

<400> 41
atgtgctgcc caaagactgc ttgcagaggt cccgtgggag tagggctgaa tgaactgaaa 60
cgaaagctgc tgatcagtga cacccagcac tatggcgtga cagtgcccca taccaccaga 120
gcaagaagaa gccaggagag tgatggtgtt gaatacattt tcatttccaa gcatttgttt 180
gagacagatg tacaaaataa caagtttatt gaatatggag aatataaaaa caactactac 240
ggcacaagta tagactcagt tcggtctgtc cttgctaaaa acaaagtttg tttgttggat 300
gttcagcctc atacagtgaa gcatttaagg acactagaat ttaagcccta tgtgatattt 360
ataaagcctc catcaataga gcgtttgaga gaaacaagaa aaaatgcaaa gattatttca 420
agcagagatg accaaggtgc tgcaaaaccc ttcacagaag aagattttca agaaatgatt 480
aaatctgcac agataatgga aagtcaatat ggtcatcttt ttgacaaaat tataataaat 540
gatgacctca ctgtggcatt caatgagctc aaaacaactt ttgacaaatt agagacagag 600
acccattggg tgccagtgag ctggttacat tcataa 636

<210> 42
<211> 211
<212> PRT
<213> homo sapiens

<400> 42
Met Cys Cys Pro Lys Thr Ala Cys Arg Gly Pro Val Gly Val Gly Leu
1 5 10 15
Asn Glu Leu Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly
20 25 30
Val Thr Val Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp
35 40 45
Gly Val Glu Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val
50 55 60
Gln Asn Asn Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr
65 70 75 80
Gly Thr Ser Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val
85 90 95
Cys Leu Leu Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu
100 105 110
Glu Phe Lys Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg
115 120 125
Leu Arg Glu Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp
130 135 140
Gln Gly Ala Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile
145 150 155 160
Lys Ser Ala Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys
165 170 175
Ile Ile Ile Asn Asp Asp Leu Thr Val Ala Phe Asn Glu Leu Lys Thr
180 185 190
Thr Phe Asp Lys Leu Glu Thr Glu Thr His Trp Val Pro Val Ser Trp
195 200 205
Leu His Ser
210

<210> 43
<211> 723
<212> DNA
<213> homo sapiens

<400> 43
atgtatgaat gcaagaagag tgatcagtac gacacagctg acgtacccac atacgaagaa 60
gtgacaccgt atcggcgaca aactaatgaa aaatacagac tcgttgtctt ggttggtccc 120
gtgggagtag ggctgaatga actgaaacga aagctgctga tcagtgacac ccagcactat 180
ggcgtgacag tgccccatac caccagagca agaagaagcc aggagagtga tggtgttgaa 240
tacattttca tttccaagca tttgtttgag acagatgtac aaaataacaa gtttattgaa 300
tatggagaat ataaaaacaa ctactacggc acaagtatag actcagttcg gtctgtcctt 360
gctaaaaaca aagtttgttt gttggatgtt cagcctcata cagtgaagca tttaaggaca 420
ctagaattta agccctatgt gatatttata aagcctccat caatagagcg tttgagagaa 480
acaagaaaaa atgcaaagat tatttcaagc agagatgacc aaggtgctgc aaaacccttc 540

acagaagaag attttcaaga aatgattaaa tctgcacaga taatggaaag tcaatatggt 600
catctttttg acaaaattat aataaatgat gacctcactg tggcattcaa tgagctcaaa 660
acaacttttg acaaattaga gacagagacc cattgggtgc cagtgagctg gttacattca 720
taa 723

<210> 44
<211> 240
<212> PRT
<213> homo sapiens

<400> 44
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
1 5 10 15
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
20 25 30
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
35 40 45
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
50 55 60
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
65 70 75 80
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
85 90 95
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
100 105 110
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
115 120 125
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
130 135 140
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
145 150 155 160
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
165 170 175
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
180 185 190
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
195 200 205
Asn Asp Asp Leu Thr Val Ala Phe Asn Glu Leu Lys Thr Thr Phe Asp
210 215 220
Lys Leu Glu Thr Glu Thr His Trp Val Pro Val Ser Trp Leu His Ser
225 230 235 240

<210> 45
<211> 1731
<212> DNA
<213> homo sapiens

<400> 45
atgccagctt tgtcaacggg atctgggagt gacactggtc tgtatgagct gttggctgct 60
ctgccagccc agctgcagcc acatgtggat agccaggaag acctgacctt cctctgggat 120
atgtttggtg aaaaaagcct gcattcattg gtaaagattc atgaaaaact acactactat 180
gagaagcaga gtccggtgcc cattctccat ggtgcggcgg ccttggccga tgatctggcc 240
gaagagcttc agaacaagcc attaaacagt gagatcagag agctgttgaa actactgtca 300
aaacccaatg tgaaggcttt gctctctgta catgatactg tggctcagaa gaattacgac 360
ccagtgttgc ctcctatgcc tgaagatatt gacgatgagg aagactcagt aaaaataatc 420
cgtctggtca aaaatagaga accactggga gctaccatta agaaggatga acagaccggg 480
gcgatcattg tggccagaat catgagagga ggagctgcag atagaagtgg tcttattcat 540
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gccaacccca gggcaggctt gatcccctca aagcatttcc aggaaaggag attggctttg 900

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<210> 46
<211> 576
<212> PRT
<213> homo sapiens

<400> 46
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Glu Asp Leu Thr Phe Leu Trp Asp Met Phe Gly Glu Lys Ser Leu His
        35                  40                  45
Ser Leu Val Lys Ile His Glu Lys Leu His Tyr Tyr Glu Lys Gln Ser
    50                  55                  60
Pro Val Pro Ile Leu His Gly Ala Ala Ala Leu Ala Asp Asp Leu Ala
65                  70                  75                  80
Glu Glu Leu Gln Asn Lys Pro Leu Asn Ser Glu Ile Arg Glu Leu Leu
                85                  90                  95
Lys Leu Leu Ser Lys Pro Asn Val Lys Ala Leu Leu Ser Val His Asp
            100                 105                 110
Thr Val Ala Gln Lys Asn Tyr Asp Pro Val Leu Pro Pro Met Pro Glu
        115                 120                 125
Asp Ile Asp Asp Glu Glu Asp Ser Val Lys Ile Ile Arg Leu Val Lys
    130                 135                 140
Asn Arg Glu Pro Leu Gly Ala Thr Ile Lys Lys Asp Glu Gln Thr Gly
145                 150                 155                 160
Ala Ile Ile Val Ala Arg Ile Met Arg Gly Gly Ala Ala Asp Arg Ser
                165                 170                 175
Gly Leu Ile His Val Gly Asp Glu Leu Arg Glu Val Asn Gly Ile Pro
            180                 185                 190
Val Glu Asp Lys Arg Pro Glu Glu Ile Ile Gln Ile Leu Ala Gln Ser
        195                 200                 205
Gln Gly Ala Ile Thr Phe Lys Ile Ile Pro Gly Ser Lys Glu Glu Thr
    210                 215                 220
Pro Ser Lys Glu Gly Lys Met Phe Ile Lys Ala Leu Phe Asp Tyr Asn
225                 230                 235                 240
Pro Asn Glu Asp Lys Ala Ile Pro Cys Lys Glu Ala Gly Leu Ser Phe
                245                 250                 255
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
            260                 265                 270
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
        275                 280                 285
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
    290                 295                 300
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
305                 310                 315                 320
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
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Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
            340                 345                 350
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
        355                 360                 365
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
    370                 375                 380
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
385                 390                 395                 400
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
                405                 410                 415
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
            420                 425                 430
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
        435                 440                 445
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
    450                 455                 460
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
465                 470                 475                 480
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
                485                 490                 495
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
            500                 505                 510
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
        515                 520                 525
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
    530                 535                 540
Asn Asp Asp Leu Thr Val Ala Phe Asn Glu Leu Lys Thr Thr Phe Asp
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Lys Leu Glu Thr Glu Thr His Trp Val Pro Val Ser Trp Leu His Ser
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<210> 47
<211> 1059
<212> DNA
<213> homo sapiens

<400> 47
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atgagccaag atgatgcaac ttggtggcaa gcgaaacacg aagctgatgc caaccccagg     180
gcaggcttga tccccctcaaa gcatttccag gaaaggagat tggctttgag acgaccagaa     240
atattggttc agcccctgaa agtttccaac aggaaatcat ctggttttag aagaagtttt     300
cgtcttagta gaaaagataa gaaaacaaat aaatccatgt atgaatgcaa gaagagtgat     360
cagtacgaca cagctgacgt acccacatac gaagaagtga caccgtatcg gcgacaaact     420
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gatgttcagc ctcatacagt gaagcattta aggacactag aatttaagcc ctatgtgata     780
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attaaatctg cacagataat ggaaagtcaa tatggtcatc tttttgacaa aattataata     960
aatgatgacc tcactgtggc attcaatgag ctcaaaacaa cttttgacaa attagagaca    1020
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<210> 48
<211> 352
<212> PRT
<213> homo sapiens

<400> 48
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            20                  25                  30
Lys Lys Gly Asp Ile Leu Gln Ile Met Ser Gln Asp Asp Ala Thr Trp
        35                  40                  45
Trp Gln Ala Lys His Glu Ala Asp Ala Asn Pro Arg Ala Gly Leu Ile
    50                  55                  60
Pro Ser Lys His Phe Gln Glu Arg Arg Leu Ala Leu Arg Arg Pro Glu
65                  70                  75                  80
Ile Leu Val Gln Pro Leu Lys Val Ser Asn Arg Lys Ser Ser Gly Phe
                85                  90                  95
Arg Arg Ser Phe Arg Leu Ser Arg Lys Asp Lys Lys Thr Asn Lys Ser
            100                 105                 110
Met Tyr Glu Cys Lys Lys Ser Asp Gln Tyr Asp Thr Ala Asp Val Pro
        115                 120                 125
Thr Tyr Glu Glu Val Thr Pro Tyr Arg Arg Gln Thr Asn Glu Lys Tyr
    130                 135                 140
Arg Leu Val Val Leu Val Gly Pro Val Gly Val Gly Leu Asn Glu Leu
145                 150                 155                 160
Lys Arg Lys Leu Leu Ile Ser Asp Thr Gln His Tyr Gly Val Thr Val
                165                 170                 175
Pro His Thr Thr Arg Ala Arg Arg Ser Gln Glu Ser Asp Gly Val Glu
            180                 185                 190
Tyr Ile Phe Ile Ser Lys His Leu Phe Glu Thr Asp Val Gln Asn Asn
        195                 200                 205
Lys Phe Ile Glu Tyr Gly Glu Tyr Lys Asn Asn Tyr Tyr Gly Thr Ser
    210                 215                 220
Ile Asp Ser Val Arg Ser Val Leu Ala Lys Asn Lys Val Cys Leu Leu
225                 230                 235                 240
Asp Val Gln Pro His Thr Val Lys His Leu Arg Thr Leu Glu Phe Lys
                245                 250                 255
Pro Tyr Val Ile Phe Ile Lys Pro Pro Ser Ile Glu Arg Leu Arg Glu
            260                 265                 270
Thr Arg Lys Asn Ala Lys Ile Ile Ser Ser Arg Asp Asp Gln Gly Ala
        275                 280                 285
Ala Lys Pro Phe Thr Glu Glu Asp Phe Gln Glu Met Ile Lys Ser Ala
    290                 295                 300
Gln Ile Met Glu Ser Gln Tyr Gly His Leu Phe Asp Lys Ile Ile Ile
305                 310                 315                 320
Asn Asp Asp Leu Thr Val Ala Phe Asn Glu Leu Lys Thr Thr Phe Asp
                325                 330                 335
Lys Leu Glu Thr Glu Thr His Trp Val Pro Val Ser Trp Leu His Ser
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<210> 49
<211> 1906
<212> DNA
<213> homo sapiens

<400> 49
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<210> 50
<211> 5426
<212> DNA
<213> homo sapiens

<400> 50
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